



PCT10

RAW SEQUENCE LISTING

DATE: 04/14/2003

PATENT APPLICATION: US/10/088,639A

TIME: 09:46:49

Input Set : N:\Cr4\04032003\J088639.raw

Output Set: N:\CRF4\04142003\J088639A.raw

1 <110> APPLICANT: Brodin, Thomas
 2 Karlstrom, Pia J.
 3 Ohlsson, Lennart G.
 4 Tordsson, Jesper M.
 5 Kearney, Philip P.
 6 Nilson, Bo H.K.
 7 <120> TITLE OF INVENTION: Novel Compounds
 8 <130> FILE REFERENCE: 003300-920
 9 <140> CURRENT APPLICATION NUMBER: US/10/088,639A
 C--> 10 <141> CURRENT FILING DATE: 1999-10-28
 11 <150> PRIOR APPLICATION NUMBER: SE 9903895-2
 12 <151> PRIOR FILING DATE: 1999-10-28
 13 <160> NUMBER OF SEQ ID NOS: 51
 14 <170> SOFTWARE: PatentIn Ver. 2.1
 16 <210> SEQ ID NO: 1
 17 <211> LENGTH: 747
 18 <212> TYPE: DNA
 19 <213> ORGANISM: Macaca fascicularis
 20 <220> FEATURE:
 21 <221> NAME/KEY: CDS
 22 <222> LOCATION: (1)..(747)
 23 <223> OTHER INFORMATION: Coding sequence VL (1-109) - modified Huston
 24 linker (110-127) - VH (128-249)
 25 <400> SEQUENCE: 1
 26 tct tct gag ctg act cag ggc cct gca ttg tct gtg gcc ttg gga cat 48
 27 Ser Ser Glu Leu Thr Gln Gly Pro Ala Leu Ser Val Ala Leu Gly His
 28 1 5 10 15
 29 aca gtc agg atg acc tgc caa gga gac agc ctc aaa acc tat tat gca 96
 30 Thr Val Arg Met Thr Cys Gln Gly Asp Ser Leu Lys Thr Tyr Tyr Ala
 31 20 25 30
 32 agc tgg tac cag cag aag cca ggc cag gtc cct gtg ctg gtc atc tat 144
 33 Ser Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Val Leu Val Ile Tyr
 34 35 40 45
 35 ggt aac aac tac cgg ccc tca ggg atc cca ggc cga ttc tct ggc tcc 192
 36 Gly Asn Asn Tyr Arg Pro Ser Gly Ile Pro Gly Arg Phe Ser Gly Ser
 37 50 55 60
 38 tgg tca gga aac aca gct tcc ttg acc atc act gcg gct cag gtg gaa 240
 39 Trp Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Ala Ala Gln Val Glu
 40 65 70 75 80
 41 gat gag gct gac tat tac tgt aac tcc tgg gac agc agc ggt acc cat 288
 42 Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Trp Asp Ser Ser Gly Thr His
 43 85 90 95
 44 ccg gta ttc ggc gga ggg acc cgg gtg acc gtc cta ggt caa gcc aac 336

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45      Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu Gly Gln Ala Asn
46              100                      105                      110
47      ggt gaa ggc ggc tct ggt ggc ggg gga tcc gga ggc ggc ggt tct gag   384
48      Gly Glu Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
49              115                      120                      125
50      gtg cag ttg gtg gag tct ggg gga ggc ttg gta aag cct ggg ggg tcc   432
51      Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
52              130                      135                      140
53      ctg aga ctc tct tgt gta gcc tct ggg tcc atc ttc agt agc tct gtt   480
54      Leu Arg Leu Ser Cys Val Ala Ser Gly Ser Ile Phe Ser Ser Ser Val
55      145                      150                      155                      160
56      atg cac tgg gtc cgc cag gct cca gga aag ggt ctg gag tgg gtc tca   528
57      Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
58              165                      170                      175
59      gtt att agt gaa aat ggg cgt acc att aac tac gca gac tct gtg aag   576
60      Val Ile Ser Glu Asn Gly Arg Thr Ile Asn Tyr Ala Asp Ser Val Lys
61              180                      185                      190
62      ggc cga ttc acc atc tcc aga gac aac gcc aag aac tca ctg ttt ctg   624
63      Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe Leu
64              195                      200                      205
65      cag atg aac agc ctg aca ggc gag gac acg gcc gtc tat tac tgt agt   672
66      Gln Met Asn Ser Leu Thr Gly Glu Asp Thr Ala Val Tyr Tyr Cys Ser
67      210                      215                      220
68      aga gag ggg gga cct gga aca acg tcc aac cgg ctc gat gcc tgg ggc   720
69      Arg Glu Gly Gly Pro Gly Thr Thr Ser Asn Arg Leu Asp Ala Trp Gly
70      225                      230                      235                      240
71      ccg gga gtc ctg gtc acc gtt tcc tca                               747
72      Pro Gly Val Leu Val Thr Val Ser Ser
73              245
75 <210> SEQ ID NO: 2
76 <211> LENGTH: 249
77 <212> TYPE: PRT
78 <213> ORGANISM: Macaca fascicularis
79 <220> FEATURE:
80 <223> OTHER INFORMATION: Coding sequence VL (1-109) - modified Huston
81      linker (110-127) - VH (128-249)
82 <400> SEQUENCE: 2
83      Ser Ser Glu Leu Thr Gln Gly Pro Ala Leu Ser Val Ala Leu Gly His
84      1                      5                      10                      15
85      Thr Val Arg Met Thr Cys Gln Gly Asp Ser Leu Lys Thr Tyr Tyr Ala
86      20                      25                      30
87      Ser Trp Tyr Gln Gln Lys Pro Gly Gln Val Pro Val Leu Val Ile Tyr
88      35                      40                      45
89      Gly Asn Asn Tyr Arg Pro Ser Gly Ile Pro Gly Arg Phe Ser Gly Ser
90      50                      55                      60
91      Trp Ser Gly Asn Thr Ala Ser Leu Thr Ile Thr Ala Ala Gln Val Glu
92      65                      70                      75                      80
93      Asp Glu Ala Asp Tyr Tyr Cys Asn Ser Trp Asp Ser Ser Gly Thr His
94      85                      90                      95

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95      Pro Val Phe Gly Gly Gly Thr Arg Val Thr Val Leu Gly Gln Ala Asn
96                100                105                110
97      Gly Glu Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu
98                115                120                125
99      Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Gly Ser
100      130                135                140
101      Leu Arg Leu Ser Cys Val Ala Ser Gly Ser Ile Phe Ser Ser Ser Val
102      145                150                155                160
103      Met His Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val Ser
104                165                170                175
105      Val Ile Ser Glu Asn Gly Arg Thr Ile Asn Tyr Ala Asp Ser Val Lys
106                180                185                190
107      Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Ser Leu Phe Leu
108                195                200                205
109      Gln Met Asn Ser Leu Thr Gly Glu Asp Thr Ala Val Tyr Tyr Cys Ser
110                210                215                220
111      Arg Glu Gly Gly Pro Gly Thr Thr Ser Asn Arg Leu Asp Ala Trp Gly
112      225                230                235                240
113      Pro Gly Val Leu Val Thr Val Ser Ser
114                245
116 <210> SEQ ID NO: 3
117 <211> LENGTH: 1073
118 <212> TYPE: PRT
119 <213> ORGANISM: Human
120 <220> FEATURE:
121 <223> OTHER INFORMATION: TA6-Human integrin alpha-6A
122 <400> SEQUENCE: 3
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125      Leu Ser Arg Leu Gly Ala Ala Phe Asn Leu Asp Thr Arg Glu Asp Asn
126                20                25                30
127      Val Ile Arg Lys Tyr Gly Asp Pro Gly Ser Leu Phe Gly Phe Ser Leu
128                35                40                45
129      Ala Met His Trp Gln Leu Gln Pro Glu Asp Lys Arg Leu Leu Leu Val
130                50                55                60
131      Gly Ala Pro Arg Gly Glu Ala Leu Pro Leu Gln Arg Ala Asn Arg Thr
132                65                70                75                80
133      Gly Gly Leu Tyr Ser Cys Asp Ile Thr Ala Arg Gly Pro Cys Thr Arg
134                85                90                95
135      Ile Glu Phe Asp Asn Asp Ala Asp Pro Thr Ser Glu Ser Lys Glu Asp
136                100                105                110
137      Gln Trp Met Gly Val Thr Val Gln Ser Gln Gly Pro Gly Gly Lys Val
138                115                120                125
139      Val Thr Cys Ala His Arg Tyr Glu Lys Arg Gln His Val Asn Thr Lys
140                130                135                140
141      Gln Glu Ser Arg Asp Ile Phe Gly Arg Cys Tyr Val Leu Ser Gln Asn
142      145                150                155                160
143      Leu Arg Ile Glu Asp Asp Met Asp Gly Gly Asp Trp Ser Phe Cys Asp
144                165                170                175

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145   Gly Arg Leu Arg Gly His Glu Lys Phe Gly Ser Cys Gln Gln Gly Val
146               180                      185                      190
147   Ala Ala Thr Phe Thr Lys Asp Phe His Tyr Ile Val Phe Gly Ala Pro
148               195                      200                      205
149   Gly Thr Tyr Asn Trp Lys Gly Ile Val Arg Val Glu Gln Lys Asn Asn
150               210                      215                      220
151   Thr Phe Phe Asp Met Asn Ile Phe Glu Asp Gly Pro Tyr Glu Val Gly
152   225                      230                      235                      240
153   Gly Glu Thr Glu His Asp Glu Ser Leu Val Pro Val Pro Ala Asn Ser
154               245                      250                      255
155   Tyr Leu Gly Phe Ser Leu Asp Ser Gly Lys Gly Ile Val Ser Lys Asp
156               260                      265                      270
157   Glu Ile Thr Phe Val Ser Gly Ala Pro Arg Ala Asn His Ser Gly Ala
158               275                      280                      285
159   Val Val Leu Leu Lys Arg Asp Met Lys Ser Ala His Leu Leu Pro Glu
160               290                      295                      300
161   His Ile Phe Asp Gly Glu Gly Leu Ala Ser Ser Phe Gly Tyr Asp Val
162   305                      310                      315                      320
163   Ala Val Val Asp Leu Asn Lys Asp Gly Trp Gln Asp Ile Val Ile Gly
164               325                      330                      335
165   Ala Pro Gln Tyr Phe Asp Arg Asp Gly Glu Val Gly Gly Ala Val Tyr
166               340                      345                      350
167   Val Tyr Met Asn Gln Gln Gly Arg Trp Asn Asn Val Lys Pro Ile Arg
168               355                      360                      365
169   Leu Asn Gly Thr Lys Asp Ser Met Phe Gly Ile Ala Val Lys Asn Ile
170               370                      375                      380
171   Gly Asp Ile Asn Gln Asp Gly Tyr Pro Asp Ile Ala Val Gly Ala Pro
172   385                      390                      395                      400
173   Tyr Asp Asp Leu Gly Lys Val Phe Ile Tyr His Gly Ser Ala Asn Gly
174               405                      410                      415
175   Ile Asn Thr Lys Pro Thr Gln Val Leu Lys Gly Ile Ser Pro Tyr Phe
176               420                      425                      430
177   Gly Tyr Ser Ile Ala Gly Asn Met Asp Leu Asp Arg Asn Ser Tyr Pro
178               435                      440                      445
179   Asp Val Ala Val Gly Ser Leu Ser Asp Ser Val Thr Ile Phe Arg Ser
180               450                      455                      460
181   Arg Pro Val Ile Asn Ile Gln Lys Thr Ile Thr Val Thr Pro Asn Arg
182   465                      470                      475                      480
183   Ile Asp Leu Arg Gln Lys Thr Ala Cys Gly Ala Pro Ser Gly Ile Cys
184               485                      490                      495
185   Leu Gln Val Lys Ser Cys Phe Glu Tyr Thr Ala Asn Pro Ala Gly Tyr
186               500                      505                      510
187   Asn Pro Ser Ile Ser Ile Val Gly Thr Leu Glu Ala Glu Lys Glu Arg
188               515                      520                      525
189   Arg Lys Ser Gly Leu Ser Ser Arg Val Gln Phe Arg Asn Gln Gly Ser
190               530                      535                      540
191   Glu Pro Lys Tyr Thr Gln Glu Leu Thr Leu Lys Arg Gln Lys Gln Lys
192   545                      550                      555                      560
193   Val Cys Met Glu Glu Thr Leu Trp Leu Gln Asp Asn Ile Arg Asp Lys

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194                               565                               570                               575
195      Leu Arg Pro Ile Pro Ile Thr Ala Ser Val Glu Ile Gln Glu Pro Ser
196                               580                               585                               590
197      Ser Arg Arg Arg Val Asn Ser Leu Pro Glu Val Leu Pro Ile Leu Asn
198                               595                               600                               605
199      Ser Asp Glu Pro Lys Thr Ala His Ile Asp Val His Phe Leu Lys Glu
200      610                               615                               620
201      Gly Cys Gly Asp Asp Asn Val Cys Asn Ser Asn Leu Lys Leu Glu Tyr
202      625                               630                               635                               640
203      Lys Phe Cys Thr Arg Glu Gly Asn Gln Asp Lys Phe Ser Tyr Leu Pro
204      645                               650                               655
205      Ile Gln Lys Gly Val Pro Glu Leu Val Leu Lys Asp Gln Lys Asp Ile
206      660                               665                               670
207      Ala Leu Glu Ile Thr Val Thr Asn Ser Pro Ser Asn Pro Arg Asn Pro
208      675                               680                               685
209      Thr Lys Asp Gly Asp Asp Ala His Glu Ala Lys Leu Ile Ala Thr Phe
210      690                               695                               700
211      Pro Asp Thr Leu Thr Tyr Ser Ala Tyr Arg Glu Leu Arg Ala Phe Pro
212      705                               710                               715                               720
213      Glu Lys Gln Leu Ser Cys Val Ala Asn Gln Asn Gly Ser Gln Ala Asp
214      725                               730                               735
215      Cys Glu Leu Gly Asn Pro Phe Lys Arg Asn Ser Asn Val Thr Phe Tyr
216      740                               745                               750
217      Leu Val Leu Ser Thr Thr Glu Val Thr Phe Asp Thr Pro Asp Leu Asp
218      755                               760                               765
219      Ile Asn Leu Lys Leu Glu Thr Thr Ser Asn Gln Asp Asn Leu Ala Pro
220      770                               775                               780
221      Ile Thr Ala Lys Ala Lys Val Val Ile Glu Leu Leu Leu Ser Val Ser
222      785                               790                               795                               800
223      Gly Val Ala Lys Pro Ser Gln Val Tyr Phe Gly Gly Thr Val Val Gly
224      805                               810                               815
225      Glu Gln Ala Met Lys Ser Glu Asp Glu Val Gly Ser Leu Ile Glu Tyr
226      820                               825                               830
227      Glu Phe Arg Val Ile Asn Leu Gly Lys Pro Leu Thr Asn Leu Gly Thr
228      835                               840                               845
229      Ala Thr Leu Asn Ile Gln Trp Pro Lys Glu Ile Ser Asn Gly Lys Trp
230      850                               855                               860
231      Leu Leu Tyr Leu Val Lys Val Glu Ser Lys Gly Leu Glu Lys Val Thr
232      865                               870                               875                               880
233      Cys Glu Pro Gln Lys Glu Ile Asn Ser Leu Asn Leu Thr Glu Ser His
234      885                               890                               895
235      Asn Ser Arg Lys Lys Arg Glu Ile Thr Glu Lys Gln Ile Asp Asp Asn
236      900                               905                               910
237      Arg Lys Phe Ser Leu Phe Ala Glu Arg Lys Tyr Gln Thr Leu Asn Cys
238      915                               920                               925
239      Ser Val Asn Val Asn Cys Val Asn Ile Arg Cys Pro Leu Arg Gly Leu
240      930                               935                               940
241      Asp Ser Lys Ala Ser Leu Ile Leu Arg Ser Arg Leu Trp Asn Ser Thr
242      945                               950                               955                               960

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VERIFICATION SUMMARY

PATENT APPLICATION: US/10/088,639A

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Input Set : N:\Crf4\04032003\J088639.raw

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L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date